In the Specification:

On page 12, please amend the paragraph beginning at line 1 as follows:

For general information regarding PFAM identifiers, PS prefix and PF prefix domain identification numbers, refer to Sonnhammer et al. (1997) *Protein* 28:405-420 and [[http://]]www.psc.edu/general/ software/packages/pfam/pfam.html.

On page 14, please amend the paragraph beginning at line 4 as follows:

As used herein, the term "carboxylesterase domain" refers to a protein domain which is includes a carboxylesterase type B signature 2 domain. Preferably, the carboxylesterase type B signature 2 domain is about 5 to 20 amino acids, more preferably 8-15, most preferably 11 amino acids and includes the sequence [EDX(0,1)CLYX]. Most preferably, the carboxylesterase type B signature 2 domain has the amino acid sequence: EDCLYNIYVP located at about amino acids 139 to 149 of SEQ ID NO:2. Preferably, the carboxylesterase domain has an amino acid sequence of about 450 to about 650 amino acid residues and having a bit score for the alignment of the sequence to the carboxylesterase domain (HMM) of at least 100. Preferably, a carboxylesterase domain includes at least about 450 to about 600 amino acids, more preferably about 500 to about 575 amino acid residues, about 550 to 570, or about 559 amino acids and has a bit score for the alignment of the sequence to the carboxylesterase domain (HMM) of at least 200, preferably 300, more preferably 400 or greater. The carboxylesterase domain (HMM) has been assigned the PFAM Accession (PF00135) ([[http://]]genome.wustl.edu/Pfam/html). An alignment of the carboxylesterase domain (from about amino acids 42 to about 601 of SEQ ID NO:2) of human 33410 with a consensus amino acid sequence derived from a hidden Markov model (PFAM) is depicted in Figure 3.

On pages 14 and 15, please amend the paragraph beginning at line 27 of page 14 as follows:

To identify the presence of an "carboxylesterase" domain in a 33410 protein sequence, and make the determination that a polypeptide or protein of interest has a particular profile, the amino acid sequence of the protein can be searched against a database of HMMs (e.g., the Pfam database, release 2.1) using the default parameters

([[http://]]www.sanger.ac.uk/Software/Pfam/HMM_search). For example, the hmmsf program, which is available as part of the HMMER package of search programs, is a family specific default program for MILPAT0063 and a score of 15 is the default threshold score for determining a hit. Alternatively, the threshold score for determining a hit can be lowered (e.g., to 8 bits). A description of the Pfam database can be found in Sonhammer *et al.* (1997) *Proteins* 28(3):405-420 and a detailed description of HMMs can be found, for example, in Gribskov *et al.*(1990) *Meth. Enzymol.* 183:146-159; Gribskov *et al.*(1987) *Proc. Natl. Acad. Sci. USA* 84:4355-4358; Krogh *et al.*(1994) *J. Mol. Biol.* 235:1501-1531; and Stultz *et al.*(1993) *Protein Sci.* 2:305-314, the contents of which are incorporated herein by reference. A search was performed against the HMM database resulting in the identification of an "carboxylesterase domain" domain in the amino acid sequence of human 33410 at about residues 42 to 601 of SEQ ID NO:2 (see Figure 1).

On page 15, please amend the paragraph beginning at line 10 as follows:

In one embodiment, a 33410 protein includes at least one transmembrane domain. As used herein, the term "transmembrane domain" includes an amino acid sequence of about 15 amino acid residues in length that spans a phospholipid membrane. More preferably, a transmembrane domain includes about at least 16, 18, 20, 21, 23, 25, 30, 35 or 40 amino acid residues and spans a phospholipid membrane. Transmembrane domains are rich in hydrophobic residues, and typically have an α-helical structure. In a preferred embodiment, at least 50%, 60%, 70%, 80%, 90%, 95% or more of the amino acids of a transmembrane domain are hydrophobic, e.g., leucines, isoleucines, tyrosines, or tryptophans. Transmembrane domains are described in, for example, [[http://]]pfam.wustl.edu/cgi-bin/getdesc?name=7tm-1, and Zagotta W.N. et al, (1996) *Annual Rev. Neuronsci.* 19: 235-63, the contents of which are incorporated herein by reference.

On page 27, please amend the paragraph beginning at line 11 as follows:

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and

Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available at [[http://]]www.gcg.com), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at [[http://]]www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A particularly preferred set of parameters (and the one that should be used if the practitioner is uncertain about what parameters should be applied to determine if a molecule is within a sequence identity or homology limitation of the invention) are a Blossum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

On pages 27 and 28, please amend the paragraph beginning at line 30 of page 27 as follows:

The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to 33410 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to 33410 protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See [[http://]]www.ncbi.nlm.nih.gov.